README

The fastq files used as input to the SORTCERY pipeline are the raw illumina reads retrieved from paired-end, deep sequencing of several pooled SORTCERY experiments. The three sets of raw files can be processed with the pipelines provided on github to demultiplex and reconstruct the distribution of clonal yeast-surface displayed cells across the FACS gates.

Link : https://github.com/KeatingLab/sortcery_design

Each set of raw files is processed by a set of scripts described by subdirectories in the git repository.

```
161011Kea_D16-11808_*_sequence.fastq  -> 2016_11_09/
140828Kea_D14-3934_*_sequence.fastq   -> SORTCERY_spec_dna
160718Kea_D16-7625_*_sequence.fastq   -> bfl1
```

Two sets of barcodes were used to identify the **experiment** and **facs gate** from which the samples were collected from.

Barcode1

24 unique inline 5-mer barcodes were used to identify the facs gate from which the sample was collected from. These barcodes are located at the 3' end of the upstream adaptor sequence and are the first 5 bases of the sequences read.

```
0 ACTCG
1 ACTGT
2 AATGC
3 AGTCA
4 ATACG
5 ATAGC
6 CGATC
7 CTAAG
8 CTCGA
9 CGAAT
10 CTGGT
11 CGGTT
12 GACTT
13 GTTCA
14 GATAC
15 GAGCA
16 GATGA
17 GTCTG
18 TCGGA
19 TGACC
20 TACTG
21 TCCAG
```

```
22 TCGAC
23 TAGCT
```

Barcode2
A set of 7 unique 6-mer barcodes identifies the experiment. These barcodes are located on the downstream adaptor.

```
0 ATCACG
1 ACAGTG
2 CGATGT
3 CAGATC
4 GATCAG
5 GCCAAT
6 TTAGGC
```

For each pipeline, the following files describe the experiment, unique_barcode_identifiers, and sortcery_gates associated with each barcode1 and barcode2 combination.

https://raw.githubusercontent.com/KeatingLab/sortcery_design/master/bfl1/workspace/mapping.txt
https://raw.githubusercontent.com/KeatingLab/sortcery_design/master/SORTCERY_spec_dna/workspace/mapping.txt
https://raw.githubusercontent.com/KeatingLab/sortcery_design/master/2016_11_09/workspace/mapping.txt

The experiments are described below:

```
Bfl1_sortcery_contam   -  Library sorted against Bfl-1 at 100 nM
Bfl1_sortcery_lowreads -  Library sorted against Bfl-1 at 100 nM
160906_x100            -  Library sorted against Bcl-xL at 100 nM
160902_x1              -  Library sorted against Bcl-xL at 1 nM
160826_m1              -  Library sorted against Mcl-1 at 1 nM
160819_f100            -  Library sorted against Bfl-1 at 100 nM
160831_m1r             -  Library sorted against Mcl-1 at 1 nM
Bcl-xl_100nM           -  Library sorted against Bcl-xL at 100 nM
BCL-xl_1nM             -  Library sorted against Bcl-xL at 1 nM
Mcl1_100nM             -  Library sorted against Mcl-1 at 100 nM
Mcl1_1nM               -  Library sorted against Mcl-1 at 1 nM
BFL1_100nM             -  Library sorted against Bfl-1 at 100 nM
Bfl1_1nM               -  Library sorted against Bfl-1 at 1 nM
```